

Fig.1

gene	polymorphism	gene	polymorphism
Angiotensin converting enzyme	I/D in intron 16	Insulin receptor substrate-1	3494G→A (Gly972Arg)
Angiotensin II type I receptor	-535C→T	Interleukin-10	-1082G→A
Angiotensinogen	-6G→A		-819T→C
Apolipoprotein A1	-75G→A		-592A→C
	83C→T	Interleukin-1 α	-889C→T
Apolipoprotein B	I/D in signal peptide	Interleukin-1 β	-511C→T
Apolipoprotein C-III	-482C→T		-3953C→T
	1100C→T	Interleukin-6	-634C→G
Apolipoprotein E	-491A→T		-174G→C
	-219G→T	LDL receptor related protein	766C→T
	3932T→C (Cys112Arg)	Leptin	-1887C→A
Apolipoprotein (a)	4070C→T (Arg158Cys)	Lipoprotein lipase	280G→A (Asp9Asn)
	93C→T		1127A→G (Asn291Ser)
	121G→A	Manganese superoxide dismutase	47C→T (Ala16Val)
	11764A→C (Thr12Pro)		173T→C (Ile58Thr)
ATP-binding cassette transporter 1	-477C→T	Matrix Gla protein	-7G→A
	1051G→A (Arg219Lys)		7158A→G (Thr83Ala)
Atrial natriuretic peptide	664G→A (Val7Met)	Metalloproteinase-1 (collagenase)	-1607G→GG
Atrial natriuretic peptide clearance receptor	-55A→C	Metalloproteinase-12 (macrophage elastase)	-82A→G
β 2-adrenergic receptor	46A→G (Arg16Gly)	Methionine synthase	2756A→G (Asp919Gly)
	79C→G (Gln27Glu)	Methylenetetrahydrofolate reductase	677C→T (Ala222Val)
	491C→T (Thr164Ile)	Monocyte chemoattractant protein-1	-2518G→A
β 3-adrenergic receptor	190T→C (Trp64Arg)	NADH/NADPH oxidase p22 phox	242C→T (His72Tyr)
β -Fibrinogen	-854G→A	Neuropeptide Y	1128T→C (Leu7Pro)
	-455G→A	Paraoxonase	-107T→C
	148C→T		172A→T (Met55Leu)
	8059G→A (Arg448Lys)		584G→A (Gln192Arg)
CD14 receptor	-260C→T	PECAM1 (CD31)	1454C→G (Leu125Val)

Fig.2

Chemokine receptor 2	190G→A (Val64Ile)	PECAM1 (CD31)	4428G→A (Ser563Asn)
Cholesterol ester transfer protein	1061A→G (Ile405Val)	Peroxisome proliferator-activated receptor-α	696C→G (Leu162Val)
	1163A→G (Asp442Gly)	Peroxisome proliferator-activated receptor-γ2	34C→G (Pro12Ala)
	1200G→A (Arg451Gln)		344C→A (Pro115Gln)
Coagulation factor V	1691G→A (Arg506Gln)	Plasminogen-activator inhibitor-1	-668/4G→5G
Coagulation factor VII	11496G→A (Arg353Glu)	Platelet-activating factor acetylhydrolase	994G→T (Val279Phe)
Coagulation factor XII	46C→T	Prothrombin	20210G→A
Coagulation factor XIII A-subunit	163G→T (Val34Leu)	P-selectin	7666A→C (Thr715Pro)
Connexin 37	1019C→T (Pro319Ser)	Scavenger receptor-BI	4G→A (Gly2Ser)
Endothelial nitric oxide synthase	-786T→C		403G→A (Val135Ile)
	894G→T (Glu298Asp)	Serotonin 2A receptor	102T→C
Endothelin-1	5665G→T (Lys198Asn)	Stromelysin-1	-1171/5A→6A
E-selectin	98G→T	Thrombomodulin	-33G→A
	561A→C (Ser128Arg)		-10GG→TA
Extracellular superoxide dismutase	1839C→T (Leu554Phe)		845G→A (Ala25Thr)
Fatty acid-binding protein 2	5775C→G (Arg213Gly)	Thrombopoietin	2136C→T (Ala455Val)
Fractalkine receptor	2445G→A (Ala54Thr)	Thrombospondin 1	5713A→G
Glycoprotein Ia	84635G→A (Val249Ile)	Thrombospondin 4	2210A→G (Asn700Ser)
	807C→T	Tissue factor pathway inhibitor	1186G→C (Ala387Pro)
	873G→A	Transforming growth factor-β1	874G→A (Val264Met)
Glycoprotein Iba	1648A→G (Lys505Glu)		-509C→T
Glycoprotein IIIa	1018C→T (Thr145Met)	Tumor necrosis factor-α	869T→C (Leu10Pro)
Glycoprotein PC-1	1565T→C (Leu33Pro)		-863C→A
G-protein β3 subunit	97A→C (Lys121Gln)		-850C→T
Hemochromatosis-associated protein	825C→T (splice variant)		-308G→A
Hepatic lipase	845G→A (Cys282Tyr)		-238G→A
	-480C→T	von Willebrand factor	-1234C→T
	-250G→A		-1051G→A

Fig.3

gene	SNP	label	primer	frequency	probe	formamide
annealing temperature, 55-67.5°C; Mg, 1-4 mM						
Platelet-activating factor acetylhydrolase	994G→T	FITC	TTCTTTTGGTGGAGCAACXGT			
		TxR	ATTCTTTTGGTGGAGCAACXIT	40		
		biotin	TCTTACCTGAATCTCTGATCTTCA			
NADH/NADPH oxidase p22 phox	242C→T	FITC	ACCACGGCGGTCAATGXGC			
		TxR	ACCACGGCGGTCAATGXAC	40		
		biotin	GCAGCAAAAGGAGTCCCGAGT			
Connexin 37	1019C→T	TxR	CTCAGAATGGCCAAAAXCC			
		FITC	CCTCAGAATGGCCAAAAXTC	35		
		biotin	GCAGAGCTGCTGGGACGA			
Angiotensinogen	-6G→A	TxR	CGGCAGCTTCTTCCCXCG			
		FITC	CGGCAGCTTCTTCCCXIG	35		
		biotin	CCACCCCTCAGCTATAAATAGG			
Tumor necrosis factor-α	-863C→A	TxR	GGCCCTGCTTCGTTAAAXGG			
		FITC	ATGGCCCTGCTTCGTTAAAXIG	35		
		biotin	CCAGGGCTATGGAAGTCGAGTATC			
Apolipoprotein C-III	-482C→T		CGGAGCCACTGATGCXCG		AGCCACTGATGCXCGGTCT	
			CGGAGCCACTGATGCXIG	35	AGCCACTGATGCXIGGTCT	30%
		biotin	TGTTTGGAGTAAAGGCACAGAA			
Interleukin-10	-592A→C	FITC	CAGAGACTGGCTTCCTACAXGA			
		TxR	CCAGAGACTGGCTTCCTACAXIA	35		
		biotin	GCCTGGAACACATCCTGTGA			

Fig.4

10/517605

Apolipoprotein E	-219G→T	FITC	GAATGGAGGAGGGTGTCTXGA		
		TxR	AGAATGGAGGAGGGTGTCTXIA	35	
		biotin	CCAGGAAGGGAGGACACCTC		
Interleukin-10	-819T→C		TACCCCTTGACAGGTGATGTAXIA		GTACAGGTGATGTAXIATCTCTGTG
			TACCCCTTGACAGGTGATGTAXCA	35	GTACAGGTGATGTAXCACTCTCTGTG
		biotin	ATAGTGAGCAAACTGAGGCACA		
Thrombospondin 4	1186G→C	TxR	CGAGTTGGGAACGCACXCT		
		FITC	CGAGTTGGGAACGCACXGT	35	
		biotin	GGTCTGCACCTGACATTGATGAG		
Paraoxonase	584G→A	FITC	ACCCAAATACATCTCCAGGAXCG		
		TxR	AACCCAAATACATCTCCAGGXCT	35	
		biotin	GAATGATATTGTTGCTGTGGGAC		
Apolipoprotein E	4070C→T	FITC	CCGATGACCTGCAGAAAXCG		
		TxR	GCCGATGACCTGCAGAAXTG	40	
		biotin	CGGCTGGTACACTGCCAG		
Plasminogen activator inhibitor-1	-668/4G→5G		GGCACAGAGAGAGTCTGGACACG		TGGACACGTGGGGGAGTCAG
		biotin	GGCCGCCTCCGATGATACA	35	TGGACACGTGGGGGAGTCAGC
Stromelysin-1	-1171/5A→6A	FITC	TTTGATGGGGGAAAAAXAC		
		TxR	TTGATGGGGGAAAAAXCC	40	
		biotin	CCTCATATCAATGTGGCCAA		
Glycoprotein Iba	1018C→T	FITC	CCCAGGGCTCCTGXCG		
		TxR	CCCCAGGGCTCCTGXIG	40	
		biotin	TGAGCTTCTCCAGCTTGGGGTG		

Fig.5

	male (n = 451)		female (n = 458)	
	control (n = 232)	myocardial infarction case (n = 219)	control (n = 232)	myocardial infarction case (n = 226)
age (years)	52.4 ± 3.6	51.8 ± 6.0	62.6 ± 8.8	62.2 ± 8.3
Body mass index (kg/m ²)	23.8 ± 2.5	24.2 ± 2.7	23.4 ± 3.2	23.2 ± 2.9
smoking (%)	60.3	60.7	9.5	16.5*1
hypertension (%)	43.5	42.9	69.8	65.5
diabetes (%)	11.2	16.0	15.5	36.7†
hypercholesterolemia (%)	45.3	52.5	59.9	66.8
hyperuricemia (%)	16.4	21.0	10.3	11.9

Fig.6

gene	polymorphism	genetic model	P	gene	polymorphism	genetic model	P
male				female			
Platelet-activating factor acetylhydrolase	994G→T	additive	0.0006	Paraoxonase	584G→A	dominant	0.009
NADH/NADPH oxidase p22 phox	242C→T	dominant	0.006	Interleukin-6	-634C→G	additive	0.009
Connexin 37	1019C→T	additive	0.007	Connexin 37	1019C→T	dominant	0.013
Thrombospondin 4	1186G→C	dominant	0.013	ATP-binding cassette transporter 1	1051G→A	additive	0.014
Angiotensinogen	-6G→A	recessive	0.019	Tumor necrosis factor-α	-850C→T	additive	0.015
Tumor necrosis factor-α	-863C→A	dominant	0.045	Endothelin-1	5665G→T	recessive	0.028
Transforming growth factor-β1	869T→C	additive	0.049	Apolipoprotein E	4070C→T	recessive	0.038
G-protein β3 subunit	825C→T	additive	0.051	Apolipoprotein C-III	-482C→T	recessive	0.044
Apolipoprotein C-III	-482C→T	recessive	0.057	Apolipoprotein E	3932T→C	dominant	0.047
Interleukin-10	-819T→C	recessive	0.061	CD14 receptor	-260C→T	additive	0.050
Thrombomodulin	2136C→T	additive	0.065	Tumor necrosis factor-α	-238G→A	dominant	0.052
Apolipoprotein E	4070C→T	additive	0.074	Plasminogen-activator inhibitor-1	-668/4G→5G	recessive	0.055
Glycoprotein Ia	A1648→G	recessive	0.080	Fatty acid-binding protein 2	2445G→A	additive	0.057
Interleukin-10	-592A→C	recessive	0.088	Insulin receptor substrate-1	3494G→A	dominant	0.058
Apolipoprotein E	-219G→T	recessive	0.092	Stromelysin-1	-1171/5A→6A	additive	0.072
Thrombopoietin	5713A→G	recessive	0.094	Glycoprotein Iba	1018C→T	additive	0.072
Apolipoprotein C-III	1100C→T	recessive	0.095	E-selectin	A561→C	dominant	0.074
Chemokine receptor 2	190G→A	recessive	0.097	Endothelial nitric oxide synthase	-786T→C	dominant	0.087
Endothelial nitric oxide synthase	-786T→C	dominant	0.098				

Fig.7

	male (n = 3309)		female (n = 1752)	
	control (n = 1306)	myocardial infarction case (n = 2003)	control (n = 936)	myocardial infarction case (n = 816)
Age (years)	60.1 ± 9.6	60.8 ± 10.3	60.8 ± 11.2	60.5 ± 10.6
Body mass index (kg/m ²)	23.6 ± 2.6	23.6 ± 2.9	23.0 ± 3.3	23.4 ± 3.5*1
Smoking (%)	57.6	58.2	9.5	15.5*2
Hypertension (%)	53.6	45.0*2	59.4	55.9
Diabetes mellitus (%)	15.4	32.4*2	16.5	42.1*1
Hypercholesterolemia (%)	35.4	43.7*2	51.2	56.8*3
Hyperuricemia (%)	17.2	14.2*3	9.7	13.2*1

Fig.8

gene	polymorphism	distribution of genotype (%)					
		control			myocardial infarction case		
male (n = 3309)							
Connexin 37	1019C→T	CC, 72.5	CT, 22.7	TT, 4.9	CC, 66.3	CT, 28.8	TT, 4.9
Tumor necrosis factor-α	-863C→A	CC, 70.9	CA, 20.7	AA, 8.5	CC, 75.5	CA, 17.9	AA, 6.6
NADH/NADPH oxidase p22 phox	242C→T	CC, 74.8	CT, 24.2	TT, 1.0	CC, 79.7	CT, 19.0	TT, 1.3
Angiotensinogen	-6G→A	GG, 2.6	GA, 29.6	AA, 67.8	GG, 4.3	GA, 33.4	AA, 62.3
Apolipoprotein E	-219G→T	GG, 8.4	GT, 42.7	TT, 48.9	GG, 7.2	GT, 39.2	TT, 53.6
Platelet-activating factor acetylhydrolase	994G→T	GG, 71.2	GT, 26.3	TT, 2.5	GG, 68.1	GT, 29.2	TT, 2.6
Apolipoprotein C-III	-482C→T	CC, 28.1	CT, 48.4	TT, 23.5	CC, 27.5	CT, 51.2	TT, 21.3
Thrombospondin 4	1186G→C	GG, 88.1	GC, 11.8	CC, 0.1	GG, 85.4	GC, 14.0	CC, 0.5
Interleukin-10	-819T→C	TT, 47.2	TC, 42.4	CC, 10.4	TT, 47.2	TC, 39.6	CC, 13.1
Interleukin-10	-592A→C	AA, 47.5	AC, 41.8	CC, 10.6	AA, 46.2	AC, 40.4	CC, 13.4
female (n = 1752)							
Stromelysin-1	-1171/5A→6A	5A/5A, 1.2	5A/6A, 47.1	6A/6A, 51.7	5A/5A, 1.8	5A/6A, 37.9	6A/6A, 60.2
Plasminogen activator inhibitor-1	-668/4G→5G	4G/4G, 43.8	4G/5G, 44.2	5G/5G, 12.0	4G/4G, 37.3	4G/5G, 49.6	5G/5G, 13.1
Glycoprotein Iba	1018C→T	CC, 76.7	CT, 20.8	TT, 2.5	CC, 77.7	CT, 21.6	TT, 0.7
Paraoxonase	584G→A	GG, 44.7	GA, 45.0	AA, 10.3	GG, 44.6	GA, 41.7	AA, 13.6
Apolipoprotein E	4070C→T	CC, 91.2	CT, 8.7	TT, 0.1	CC, 91.8	CT, 7.2	TT, 1.0

Fig.9

gene	polymorphism	Dominant		Recessive		Additive	
		P	OR (95% CI)	P	OR (95% CI)	P	OR (95% CI)
male (n = 3309)							
Connexin 37	1019C→T	0.0001	1.4 (1.2-1.7)	0.7834		<0.0001	1.5 (1.2-1.7)
Tumor necrosis factor-α	-863C→A	0.0020	0.7 (0.6-0.9)	0.0235	0.7 (0.5-1.0)	0.0105	0.7 (0.5-0.9)
NADH/NADPH oxidase p22 phox	242C→T	0.0027	0.7 (0.6-0.9)	0.9462		0.0021	0.7 (0.6-0.9)
Angiotensinogen	-6G→A	0.0563		0.0038	0.8 (0.7-0.9)	0.0283	0.6 (0.4-0.9)
Apolipoprotein E	-219G→T	0.4015		0.0085	1.2 (1.1-1.4)	0.1557	
Platelet-activating factor acetylhydrolase	994G→T	0.0349	1.2 (1.0-1.4)	0.6522		0.0227	1.2 (1.0-1.4)
Apolipoprotein C-III	-482C→T	0.6297		0.0367	0.8 (0.7-1.0)	0.2716	
Thrombospondin 4	1186G→C	0.0373	1.3 (1.0-1.6)	0.0834		0.0700	
Interleukin-10	-819T→C	0.9108		0.0375	1.3 (1.0-1.6)	0.0738	
Interleukin-10	-592A→C	0.2692		0.0427	1.3 (1.0-1.6)	0.0394	1.3 (1.0-1.7)
female (n = 1752)							
Stromelysin-1	-1171/5A→6A	<0.0001	2.1 (1.6-2.8)	0.0002	1.5 (1.2-1.9)	<0.0001	2.2 (1.6-2.9)
Plasminogen activator inhibitor-1	-668/4G→5G	0.0008	1.5 (1.2-1.8)	0.4495		0.0010	1.5 (1.2-1.9)
Glycoprotein Iba	1018C→T	0.6065		0.0238	0.3 (0.1-0.8)	0.0242	0.3 (0.1-0.8)
Paraoxonase	584G→A	0.3966		0.0349	1.4 (1.0-2.0)	0.1017	
Apolipoprotein E	4070C→T	0.6881		0.0399	9.7 (1.6-185.6)	0.0418	9.5 (1.6-181.7)

Fig.10

gene	locus	polymorphism	genetic model	P	odds ratio	95% CI
<u>male</u>						
Connexin 37	1p35.1	1019C→T	TT + CT versus CC	0.0124	1.31	1.06-1.61
Tumor necrosis factor- α	6p21.3	-863C→A	AA + CA versus CC	0.0336	0.79	0.64-0.98
NADH/NADPH oxidase p22 phox	16q24	242C→T	TT + CT versus CC	0.2926	0.88	0.70-1.11
Angiotensinogen	1q42-q43	-6G→A	AA versus GA + GG	0.0251	0.79	0.65-0.97
Apolipoprotein E	19q13.2	-219G→T	TT versus GT + GG	0.0209	1.26	1.03-1.51
Platelet-activating factor acetylhydrolase	6p21.2-p12	994G→T	TT + GT versus GG	0.0155	1.30	1.05-1.59
Apolipoprotein C-III	11q23	-482C→T	TT versus CT + CC	0.0606	0.80	0.64-1.01
Thrombospondin 4	5q13	1186G→C	CC + GC versus GG	0.0011	1.64	1.22-2.21
Interleukin-10	1q31-q32	-819T→C	CC versus CT + TT	0.5643	1.20	0.65-2.17
Interleukin-10	1q31-q32	-592A→C	CC versus CA + AA	0.6323	1.16	0.63-2.12
<u>female</u>						
Stromelysin-1	11q23	-1171/5A→6A	6A/6A + 5A/6A versus 5A/5A	<0.0001	1.87	1.42-2.47
Plasminogen activator inhibitor-1	7q21.3-q22	-668/4G→5G	5G/5G + 4G/5G versus 4G/4G	0.0005	1.50	1.19-1.89
Glycoprotein Iba	22q11.2	1018C→T	TT versus CT + CC	0.0308	0.28	0.09-0.89
Paraoxonase	7q21.3	584G→A	AA versus GA + GG	0.1889	1.27	0.89-1.81
Apolipoprotein E	19q13.2	4070C→T	TT versus CT + CC	0.0872	6.96	0.75-64.36

Fig.11

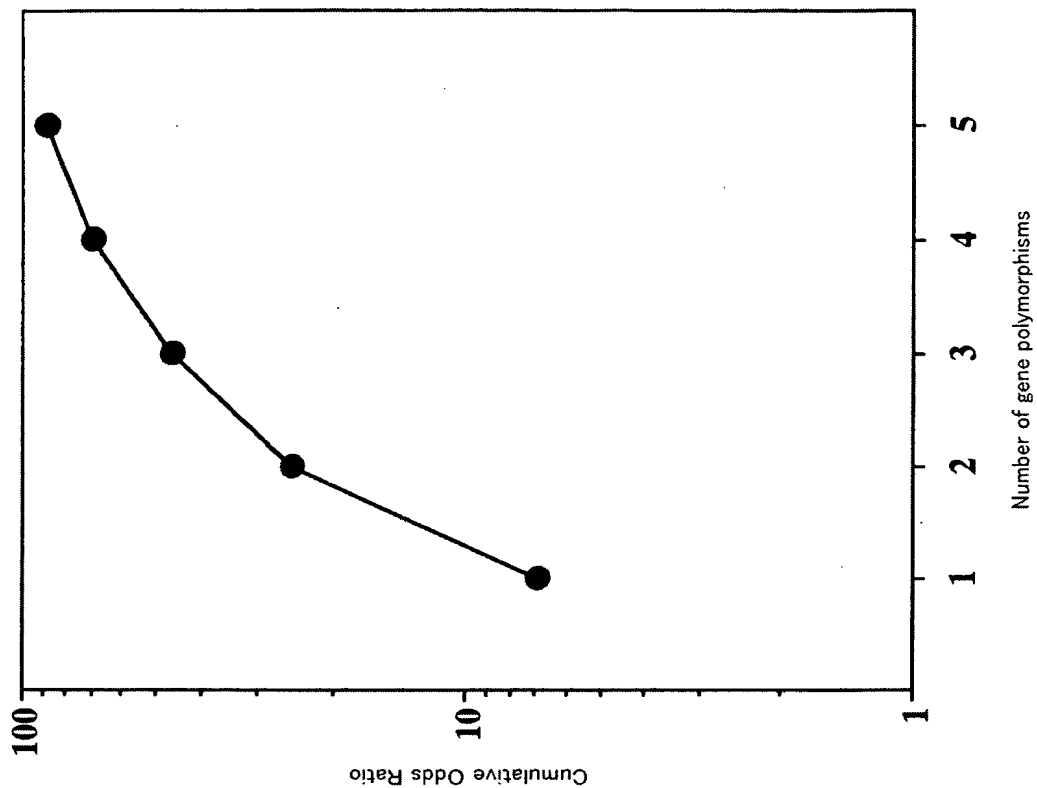
Thrombospondin 4 (0 = GG, 1 = GC = CC)	Connexin 37 (0 = CC, 1 = CT = TT)	Platelet-activating factor acetylhydrolase (0 = GG, 1 = GT = TT)	Angiotensinogen (0 = GA = GG, 1 = AA)	Tumor necrosis factor- α (0 = CC, 1 = CA = AA)	odds ratio
1	1	1	0	0	4.50
1	1	1	0	1	3.55
1	1	1	1	0	3.55
1	1	1	1	1	2.79
1	1	0	0	0	3.47
1	1	0	0	1	2.73
1	1	0	1	0	2.73
1	1	0	1	1	2.15
1	0	1	0	0	3.44
1	0	1	0	1	2.71
1	0	1	1	0	2.71
1	0	1	1	1	2.13
1	0	0	0	0	2.65
1	0	0	0	1	2.08
1	0	0	1	0	2.08
1	0	0	1	1	1.64
0	1	1	0	0	2.75
0	1	1	0	1	2.16
0	1	1	1	0	2.16
0	1	1	1	1	1.70
0	1	0	0	0	2.11
0	1	0	0	1	1.66
0	1	0	1	0	1.66
0	1	0	1	1	1.31
0	0	1	0	0	2.10
0	0	1	0	1	1.65
0	0	1	1	0	1.65
0	0	1	1	1	1.30
0	0	0	0	0	1.61
0	0	0	0	1	1.27
0	0	0	1	0	1.27
0	0	0	1	1	1.00

Fig.12

Apolipoprotein E (0 = CC = CT, 1 = TT)	Glycoprotein Iba (0 = CC = CT, 1 = TT)	Stromelysin-1 (0 = 5A/5A, 1 = 5A/6A = 6A/6A)	Plasminogen activator inhibitor-1 (0 = 4G/4G, 1 = 4G/5G = 5G/5G)	Paraoxonase (0 = GG = GA, 1 = AA)	odds ratio
1	0	1	1	1	88.51
1	0	1	1	0	69.70
1	0	1	0	1	59.01
1	0	1	0	0	46.46
1	0	0	1	1	47.33
1	0	0	1	0	37.27
1	0	0	0	1	31.56
1	0	0	0	0	24.85
1	1	1	1	1	24.79
1	1	1	1	0	19.52
1	1	1	0	1	16.53
1	1	1	0	0	13.02
1	1	0	1	1	13.26
1	1	0	1	0	10.44
1	1	0	0	1	8.84
1	1	0	0	0	6.96
0	0	1	1	1	12.72
0	0	1	1	0	10.01
0	0	1	0	1	8.48
0	0	1	0	0	6.68
0	0	0	1	1	6.80
0	0	0	1	0	5.36
0	0	0	0	1	4.53
0	0	0	0	0	3.57
0	1	1	1	1	3.56
0	1	1	1	0	2.81
0	1	1	0	1	2.37
0	1	1	0	0	1.87
0	1	0	1	1	1.91
0	1	0	1	0	1.50
0	1	0	0	1	1.27
0	1	0	0	0	1.00

Fig.13

(B)



(A)

